<110> Cahoon, Rebecca
Gutteridge, Steven
Lee, Jian-Ming
McGonigle, Brian
Rafalski, Antoni

<120> Ornithine Biosynthesis Enzymes

<130> BB-1174

<140> 09/744,100
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<150> PCT/US99/15931
<151> 1999-07-14

<150> 60/093,209
<151> 1998-07-17

<160> 12

<170> Microsoft Office 97

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<211> 1201
<212> DNA
<213> Zea mays

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tgcaagcccc cttgccgccc ctacttgccg tcgcagccgc ctccgcatct ccgccacatc 180
cacggctgcg ccgtctcctt cgtcggctgc cgctgccacc gcgtcgctga gtcgagtgga 240
cgtgctctcg gaggcgctcc cttttattca gcgattcaaa ggcaagacgg tggtggtcaa 300
gtacggcggt gcggcgatga agtccccgga gctgcaggcg tccgtgatcc gcgatctcgt 360
gctgctctcc tgcgtcggcc tccgccccgt gcttgttcac ggcggcggtc cggagattaa 420
ttcctggctg ctgcgcgtcg gcgtcgagcc gcagttccgc gacggcctcc gcgtcacgga 480
cgcgctcacc atggaggtcg tcgagatggt gctagtcggg aaggtcaaca aaaaccttgt 540
ttccctcatc aacatcgcgg gaggcaccgc cattggtctg tgcggcaagg acgcgcgcct 600
tatcaccgct cgcccgtctc caaatgcagc ggcgctggga ttcgtcggcg aggtttcgcg 660
cgtggacgcc accgtcctcc atcccatcat cgccgcgggc catatcccgg ttatcgccac 720
cgttgccgcc gacgagactg ggcaagccta taacatcaat gctgatacgg cggctggcga 780
gattgccgct gccgtgggcg ccgagaagct gctgttgctc acagatgtgt ctggcatttt 840
ggcggaccgt aatgaccctg ggagcctggt gaaggtggtc gacattgctg gggtgcggaa 900
gatggtggct gacgggaagg tagctggtgg gatgataccc aaggtggagt gttgtgttca 960
cgcccttgca caaggtgtac acaccgcaag tatcattgat gggcgtgttc cacactctct 1020
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atgccttcat ggtattttcc tgtgcctctt ttctcatatt gttgtgtttt atggctatgt 1140
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a 1201

<210> 2
<211> 345
<212> PRT
<213> Zea mays

<400> 2
Met Leu Leu Thr Lys Pro Tyr Leu Ser Asn Ser Leu Leu Pro Val Pro
1 5 10 15

Ser Pro Pro Pro Ser Gly Pro Thr Leu Ser Ser Asn His Ala Ser Pro
20 25 30

Leu Ala Ala Pro Thr Cys Arg Arg Ser Arg Leu Arg Ile Ser Ala Thr
35 40 45

Ser Thr Ala Ala Pro Ser Pro Ser Ser Ala Ala Ala Ala Thr Ala Ser
50 55 60

Leu Ser Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg
65 70 75 80

Phe Lys Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys
85 90 95

Ser Pro Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser
100 105 110

Cys Val Gly Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile
115 120 125

Asn Ser Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asp Gly
130 135 140

Leu Arg Val Thr Asp Ala Leu Thr Met Glu Val Val Glu Met Val Leu
145 150 155 160

Val Gly Lys Val Asn Lys Asn Leu Val Ser Leu Ile Asn Ile Ala Gly
165 170 175

Gly Thr Ala Ile Gly Leu Cys Gly Lys Asp Ala Arg Leu Ile Thr Ala
180 185 190

Arg Pro Ser Pro Asn Ala Ala Ala Leu Gly Phe Val Gly Glu Val Ser
195 200 205

Arg Val Asp Ala Thr Val Leu His Pro Ile Ile Ala Ala Gly His Ile
210 215 220

Pro Val Ile Ala Thr Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn
225 230 235 240

Ile Asn Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala
245 250 255

Glu Lys Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg
260 265 270

Asn Asp Pro Gly Ser Leu Val Lys Val Val Asp Ile Ala Gly Val Arg
275 280 285

Lys Met Val Ala Asp Gly Lys Val Ala Gly Gly Met Ile Pro Lys Val
290 295 300

Glu Cys Cys Val His Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile
305 310 315 320

Ile Asp Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp
325 330 335

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Glu Gly Thr Gly Thr Met Ile Thr Gly
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<210> 3
<211> 1186
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (613)
<223> n = A, C, G, or T

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ctctttcctc ccatccacgc gggtgtctag ccccgctccg ggtcccaacc acgcaaagcc  120
catcgccgcc tctcccgccc ctcgacgctg cctccgtctc gccgtcacat ccgccgcggc  180
gccggctgct tcgtcggcgg aggcggcggc ggcgctgagc cgcgtggatg tgctctcaga  240
ggcgctcccc ttcatccagc gcttcaaggg gaagaccgtg gtggtgaagt acggcggcgc  300
ggcgatgaag tcgccggagc tccaggcttc agtgatccgc gacctggtcc tcctctcgtg  360
cgtcggcctc caccccgtgc tcgtccacgg cggcgggccc gagatcaact cctggctgct  420
ccgcgtcggc gtcgagccgc agttccggaa cggcctccgc gtcactgacg cgctcaacat  480
ggaggtcgtc gagatggtgc tcgtccgcaa ggtcaacaaa gaactcctct ccctcatcaa  540
actcccgggg gggagcgccg taagtctctg ttggaaggaa gctcgcctcc tcaacgagcg  600
gccctccccg aangaaaagg gccttcggtt tgtcggcggg gtctggcgcg tggacgccac  660
cgtcctccac ccaatcatcg cctccggtca catcccggtc atcgccactg tgggcgccga  720
cgagaccggg caggcctaca acatcaacgc tgacacggcg gccggcgaga tcgccgccgc  780
ggtcggcgcg gagaagctgt tgctgctcac agatgtgtct ggaattctgg ccgaccgtaa  840
tgaccccggg agtctggtga aagagatcga cattgctggg gtgcggcaga tggtggccga  900
cgggcaggta gctggtggga tgataccgaa ggtggaatgc tgcgtgcgtg ccctcgcaca  960
gggcgtgcac actgcaagca tcatcgatgg gcgtgtcccg cactcgttgc tgctcgagat 1020
tctcacagat gagggcactg gcactatgat cactggctga ggtgattcat cccgtcgtgg 1080
tattctccgg tgcctctctt ctcatactgt aatgtaattt gcatttgata tgcctcatga 1140
ttgcaataag aattgtattc ctcaaaaaaa aaaaaaaaaa aaaaaa                 1186

<210> 4
<211> 343
<212> PRT
<213> Oryza sativa

<220>
<221> UNSURE
<222> (195)
<223> Xaa = ANY AMINO ACID

<400> 4
Met Leu Leu Ala Lys Pro His Leu Ser Ser Ser Ser Phe Leu Pro Ser
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Thr Arg Val Ser Ser Pro Ala Pro Gly Pro Asn His Ala Lys Pro Ile
             20                  25                  30

Ala Ala Ser Pro Ala Pro Arg Arg Cys Leu Arg Leu Ala Val Thr Ser
         35                  40                  45

Ala Ala Ala Pro Ala Ala Ser Ser Ala Glu Ala Ala Ala Ala Leu Ser
     50                  55                  60

Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys
 65                  70                  75                  80
```

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Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro
                 85                  90                  95

Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val
            100                 105                 110

Gly Leu His Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser
        115                 120                 125

Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asn Gly Leu Arg
    130                 135                 140

Val Thr Asp Ala Leu Asn Met Glu Val Val Glu Met Val Leu Val Arg
145                 150                 155                 160

Lys Val Asn Lys Glu Leu Leu Ser Leu Ile Lys Leu Pro Gly Gly Ser
                165                 170                 175

Ala Val Ser Leu Cys Trp Lys Glu Ala Arg Leu Leu Asn Glu Arg Pro
            180                 185                 190

Ser Pro Xaa Glu Lys Gly Leu Arg Phe Val Gly Gly Val Trp Arg Val
        195                 200                 205

Asp Ala Thr Val Leu His Pro Ile Ile Ala Ser Gly His Ile Pro Val
    210                 215                 220

Ile Ala Thr Val Gly Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn
225                 230                 235                 240

Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala Glu Lys
                245                 250                 255

Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp
            260                 265                 270

Pro Gly Ser Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met
        275                 280                 285

Val Ala Asp Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys
    290                 295                 300

Cys Val Arg Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp
305                 310                 315                 320

Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly
                325                 330                 335

Thr Gly Thr Met Ile Thr Gly
            340
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<210> 5
<211> 1204
<212> DNA
<213> Glycine max

<400> 5
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cccaaccaaa ccccaaaacc aactcaccac tagccacgct ttcccttcca ctcgcctccg 120
ccaccgcgcc atttccgcgg tggcgaacgc ggcgcaacct ccactcgccg ccgccactgc 180
caccgagggt cagtaccgag tcgatgtgct ctcggagtcg ctccccttca tccagaaatt 240

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ccgcggcaaa accatcgtcg tcaagtacgg cggcgccgcc atgaagtccc cggagctcca  300
ggcctccgtg atcaacgacc ttgtcctcct ctcctgcgtc ggcctccgcc ccgtcctggt  360
ccacggcggc ggccccgaga tcaactcctg gctcggccgc ctcaacatcc ccgccgtctt  420
ccgcgacggc ctccgcgtca ccgacgccga caccatggag atcgtctcca tggtcctcgt  480
cggaaaagtc aacaaaaccc tagtttctct aattaacaag gccggcgcca ccgccgtcgg  540
cctctctggc atggacggcc gcctcctcac cgcccgcccc gctcccaagg ccgccgacct  600
cggctacgtc ggcgaggtcg cacgcgtcga tcccgccgtc ctccgctccc taatcgacac  660
cagccacatc cccgtcgtca cctccgtcgc cgccgatgaa tccggacagc cctacaacat  720
caacgccgac accgtcgccg gagaattggc agcgtcgctc ggcgcggaga agctgattct  780
gctgaccgat gtggcgggaa ttctggaaga tcggaacgac cctgacagct tggtgaagaa  840
gattgacata aaaggagtga agaaaatgat ggaagatgga aaagttggtg gtggaatgat  900
acctaaggtt aattgttgcg ttaggtcctt ggcgcaaggg gttattacag cgagtattat  960
tgatggtagg gttccgcatt ctttgttgct tgagattttg actgatgaag gtgctggaac 1020
tatgataact ggataagttt atttatttat ggtgtttgga ttttttcttt tcaatcaagc 1080
cttgagttga ggttgcattg cagcacttgt tttgttagag attggtgatt gtttttaagt 1140
gcgtgtaatg tgagagatgg ttgaattgaa ttgaatgttt cagaaaaaaa aaaaaaaaaa 1200
aaaa                                                              1204
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<210> 6
<211> 342
<212> PRT
<213> Glycine max

<400> 6

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Met Met Ala Gly Ala Ala Lys Thr Leu Thr Asn Leu Cys Pro Ser Phe
  1               5                  10                  15

Pro Phe Pro Thr Lys Pro Gln Asn Gln Leu Thr Thr Ser His Ala Phe
            20                  25                  30

Pro Ser Thr Arg Leu Arg His Arg Ala Ile Ser Ala Val Ala Asn Ala
        35                  40                  45

Ala Gln Pro Pro Leu Ala Ala Ala Thr Ala Thr Glu Gly Gln Tyr Arg
    50                  55                  60

Val Asp Val Leu Ser Glu Ser Leu Pro Phe Ile Gln Lys Phe Arg Gly
65                  70                  75                  80

Lys Thr Ile Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu
                85                  90                  95

Leu Gln Ala Ser Val Ile Asn Asp Leu Val Leu Leu Ser Cys Val Gly
            100                 105                 110

Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp
        115                 120                 125

Leu Gly Arg Leu Asn Ile Pro Ala Val Phe Arg Asp Gly Leu Arg Val
    130                 135                 140

Thr Asp Ala Asp Thr Met Glu Ile Val Ser Met Val Leu Val Gly Lys
145                 150                 155                 160

Val Asn Lys Thr Leu Val Ser Leu Ile Asn Lys Ala Gly Ala Thr Ala
                165                 170                 175

Val Gly Leu Ser Gly Met Asp Gly Arg Leu Leu Thr Ala Arg Pro Ala
            180                 185                 190

Pro Lys Ala Ala Asp Leu Gly Tyr Val Gly Glu Val Ala Arg Val Asp
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```
        195                 200                 205

Pro Ala Val Leu Arg Ser Leu Ile Asp Thr Ser His Ile Pro Val Val
    210                 215                 220

Thr Ser Val Ala Ala Asp Glu Ser Gly Gln Pro Tyr Asn Ile Asn Ala
225                 230                 235                 240

Asp Thr Val Ala Gly Glu Leu Ala Ala Ser Leu Gly Ala Glu Lys Leu
                245                 250                 255

Ile Leu Leu Thr Asp Val Ala Gly Ile Leu Glu Asp Arg Asn Asp Pro
        260                 265                 270

Asp Ser Leu Val Lys Lys Ile Asp Ile Lys Gly Val Lys Lys Met Met
        275                 280                 285

Glu Asp Gly Lys Val Gly Gly Gly Met Ile Pro Lys Val Asn Cys Cys
    290                 295                 300

Val Arg Ser Leu Ala Gln Gly Val Ile Thr Ala Ser Ile Ile Asp Gly
305                 310                 315                 320

Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Ala
                325                 330                 335

Gly Thr Met Ile Thr Gly
            340
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<210> 7
<211> 1246
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (492)..(542)
<223> n = A, C, G, or T

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ctaacctaaa ggccgcccgc gtcaggcccc tcgcctcctc cgcgccccat ggacgccgcg  180
ggctccgcgt ctcggcctcc tcctcctccc tggcgccagc gcaggccgcg tccgcggcgc  240
tgaaccgcgt ggacgtcctg tcggaggcgc tccccttcat ccagcggttc aagggcaaga  300
cggtggtggt caagtacggc ggcgcggcca tgaagtcgcc ggagctgcag gcgtcggtga  360
tccgcgacct ggtcctcctc tcctgcgtcg gcctgcgccc cgtgctcgtg cacggcggcg  420
gcccggagat caactcctgg ctgcagcgcg tcggggtcta gccgcagttc cgcaacggcc  480
tccgcgtcac gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  540
nnaagcagct cttatcccta atcaggcctg cggggaccac agcagttggc ctctgcagaa  600
aggacgggcg catcctaacg gagcgccccc ccccagacgc cgcagccctc gggttcgtcg  660
gcgaggtcac gagaaaaaac ccctctgtgc tccacccgat catcgcctcc agccacatcc  720
cggtcatcgc caccgtggct gccgacgaga ccgggcaagc ctataacatc aacgctgaca  780
ctgcggcggg ggagatcgcg gctgccattg gcgccgagaa gctgttgctg atcactgacg  840
tgtccggcat actcgcggac cgggatgacc ccgggagcct ggtgaaggag attgacatcg  900
ccggcgtacg gcggatggtg gccgagggca aggtgggtgg gggcatgata cccaaggtgg  960
ggtgctgcgt gcgcgcgctg gcgcagggcg tgcacacggc cagcatcatt gacggccgcg 1020
tcccgcactc tctcctgctc gaaatcctca ccgacgaggg caccggcacc atgatcaccg 1080
gctgaaactt gtttgtttgt tgttgttttt ttcttttctt ttttggttca cattctttgg 1140
gttggatggt tttgcatccc tcatttgtgt taaatgtgtt ttcgattcga atcctgaaca 1200
aggagtggtg aaagattgca gctttaagca aaaaaaaaaa aaaaaa                 1246
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<210> 8
<211> 340
<212> PRT
<213> Triticum aestivum

<220>
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<222> (133)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (144)..(160)
<223> Xaa = ANY AMINO ACID

<400> 8

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Met Leu Leu Thr Lys Pro His Pro Ala Leu Thr Leu Pro Ser Ala Ser
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Leu Pro Asn Pro Asn Leu Lys Ala Ala Arg Val Arg Pro Leu Ala Ser
             20                  25                  30

Ser Ala Pro His Gly Arg Arg Gly Leu Arg Val Ser Ala Ser Ser Ser
         35                  40                  45

Ser Leu Ala Pro Ala Gln Ala Ala Ser Ala Ala Leu Asn Arg Val Asp
     50                  55                  60

Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys Gly Lys Thr
 65                  70                  75                  80

Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu Leu Gln
                 85                  90                  95

Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val Gly Leu Arg
            100                 105                 110

Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp Leu Gln
        115                 120                 125

Arg Val Gly Val Xaa Pro Gln Phe Arg Asn Gly Leu Arg Val Thr Xaa
    130                 135                 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145                 150                 155                 160

Lys Gln Leu Leu Ser Leu Ile Arg Pro Ala Gly Thr Thr Ala Val Gly
                165                 170                 175

Leu Cys Arg Lys Asp Gly Arg Ile Leu Thr Glu Arg Pro Ser Pro Asp
            180                 185                 190

Ala Ala Ala Leu Gly Phe Val Gly Glu Val Thr Arg Lys Asn Pro Ser
        195                 200                 205

Val Leu His Pro Ile Ile Ala Ser Ser His Ile Pro Val Ile Ala Thr
    210                 215                 220

Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn Ala Asp Thr
225                 230                 235                 240
```

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Ala Ala Gly Glu Ile Ala Ala Ala Ile Gly Ala Glu Lys Leu Leu Leu
                245                 250                 255

Ile Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asp Asp Pro Gly Ser
            260                 265                 270

Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Arg Met Val Ala Glu
        275                 280                 285

Gly Lys Val Gly Gly Gly Met Ile Pro Lys Val Gly Cys Cys Val Arg
    290                 295                 300

Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp Gly Arg Val
305                 310                 315                 320

Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Thr Gly Thr
                325                 330                 335

Met Ile Thr Gly
            340
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<210> 9
<211> 439
<212> DNA
<213> Triticum aestivum

<400> 9
gcacgaggtg agattgccgc tgcggtgggc gccgagaaat tgctactgct cacagatgtg 60
tctgggatac tggcggaccg taatgaccct ggcagcctgg tgaaggagat tgacatcgct 120
ggggtgcggc agatggtatc cggtgggcag gttgctggtg gaatgatccc aaaggtggag 180
tgctgcgtga gagccctcgc ccagggtgtg cacactgcaa gcatcatcga tgggcgtgtc 240
ccgcactcgc tgttgctcga gattctcaca gatgagggca ctggcacaat gatcaccggc 300
taaggtgtaa aatgcctcct tggtacttcc ttatgccttt ctgttcatac tgccaatctg 360
ccatgtaatt tatgccaatg tagcctcacc tcatgattgc aataagagta ccttcctgac 420
aaaaaaaaaa aaaaaaaaa   439

<210> 10
<211> 100
<212> PRT
<213> Triticum aestivum

<400> 10
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Ala Arg Gly Glu Ile Ala Ala Ala Val Gly Ala Glu Lys Leu Leu Leu
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Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp Pro Gly Ser
             20                  25                  30

Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met Val Ser Gly
         35                  40                  45

Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys Cys Val Arg
     50                  55                  60

Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp Gly Arg Val
 65                  70                  75                  80

Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Thr Gly Thr
                 85                  90                  95
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Met Ile Thr Gly
100

<210> 11
<211> 297
<212> PRT
<213> Synechocystis sp.

<400> 11
Met Ser Ser Thr Gln Asp Tyr Ile Gly Glu Glu Ala Ala Thr Arg Val
1 5 10 15

Lys Ile Leu Ser Glu Ala Leu Pro Tyr Ile Gln His Phe Ala Gly Arg
20 25 30

Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Asp Ser Asn Leu
35 40 45

Lys Asp Lys Val Ile Arg Asp Ile Val Phe Met Ala Ser Val Gly Ile
50 55 60

Arg Pro Val Val Val His Gly Gly Gly Pro Glu Ile Asn Thr Trp Leu
65 70 75 80

Asp Lys Val Gly Ile Glu Pro Gln Phe Lys Asp Gly Leu Arg Val Thr
85 90 95

Asp Ala Ala Thr Met Asp Ile Val Glu Met Val Leu Val Gly Arg Val
100 105 110

Asn Lys Glu Leu Val Asn Leu Ile Asn Gln Ala Gly Gly Lys Ala Val
115 120 125

Gly Leu Cys Gly Lys Asp Gly Gln Leu Met Thr Ala Arg Thr Met Thr
130 135 140

Asn Lys Asp Val Gly Phe Val Gly Glu Val Ser Ser Val Asp Ala Arg
145 150 155 160

Val Val Glu Thr Leu Val Lys Ser Gly Tyr Ile Pro Val Ile Ser Ser
165 170 175

Val Ala Ala Asp Glu Phe Gly Gln Ala His Asn Ile Asn Ala Asp Thr
180 185 190

Cys Ala Gly Glu Leu Ala Ala Ala Leu Gly Ala Glu Lys Leu Ile Leu
195 200 205

Leu Thr Asp Thr Arg Gly Ile Leu Arg Asp Tyr Lys Asp Pro Ser Thr
210 215 220

Leu Ile His Lys Leu Asp Ile Gln Gln Ala Arg Glu Leu Ile Gly Ser
225 230 235 240

Gly Ile Val Ala Gly Gly Met Ile Pro Lys Val Thr Cys Cys Val Arg
245 250 255

Ser Leu Ala Gln Gly Val Arg Ala Ala His Ile Leu Asp Gly Arg Leu
260 265 270

Pro His Ala Leu Leu Leu Glu Val Phe Thr Asp Leu Gly Ile Gly Ser

275 280 285

Met Ile Val Ala Ser Gly Tyr Asp Leu
290 295

<210> 12
<211> 346
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CONSENSUS

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<222> (2)
<223> Xaa = Leu OR Met

<220>
<221> UNSURE
<222> (3)
<223> Xaa = Leu OR Ala

<220>
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<222> (4)
<223> Xaa = Thr, Ala, OR Gly

<220>
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<222> (5)
<223> Xaa = Lys OR NONE

<220>
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<222> (6)
<223> Xaa = Pro OR NONE

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<222> (8)
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<222> (9)
<223> Xaa = Ser, Ala, OR NONE

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<222> (10)
<223> Xaa = Asn, Ser, Ala, OR NONE

<220>
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<222> (11)
<223> Xaa = Ser, Lys, OR Pro

<220>
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<222> (12)
<223> Xaa = Leu, Ser, Thr, OR Ala

<220>
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<222> (13)
<223> Xaa = Leu OR Phe

<220>
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<222> (14)
<223> Xaa = Pro, Thr, OR NONE

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<220>
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<222> (16)
<223> Xaa = Pro OR Leu

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<223> Xaa = Ser OR Cys

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<222> (18)
<223> Xaa = Pro, Thr, OR Ala

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<222> (20)
<223> Xaa = Pro, Val, Phe, OR Leu

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<222> (21)
<223> Xaa = Ser ORPro

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<223> Xaa = Gly, Ser, Phe, OR Asn

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<223> Xaa = Leu, Pro, OR Lys

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<223> Xaa =Ser, Pro, Gln, OR Ala

<220>
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<222> (28)
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